

GenCore version 6.3
Copyright (c) 1993 - 2009 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 26, 2009, 03:22:05 ; Search time 20 Seconds
(without alignments)
20013.649 Million cell
updates/sec

Title: US-09-300-482-225
Perfect score: 316
Sequence: 1
gataaggtgcgcacactgag.....gaatggaggaggagtacttcga 316

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1681669 seqs, 647077473 residues

Total number of hits satisfying chosen parameters: 3363338

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_New:*
1:
/ABSS/Data/CRF/ptodata/2/pubpna/US09_NEW_PUB.seq:*
2:
/ABSS/Data/CRF/ptodata/2/pubpna/US10_NEW_PUB.seq:*
3:
/ABSS/Data/CRF/ptodata/2/pubpna/US11_NEW_PUB.seq:*
4:
/ABSS/Data/CRF/ptodata/2/pubpna/US12_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to
have a
score greater than or equal to the score of the result being
printed,
and is derived by analysis of the total score distribution.